

- (a) preparing a library of DNA or RNA sequences from a non-plant donor organism, and constructing recombinant viral nucleic acids each comprising an unidentified nucleic acid insert obtained from said library in a positive sense orientation;
- (b) infecting plant hosts with said recombinant viral nucleic acids;
- X (c) transiently expressing the unidentified nucleic acid inserts in said infected plant hosts;
- (d) determining one or more phenotypic or biochemical changes in said plant hosts;
- (e) correlating said one or more phenotypic or biochemical changes to a host plant that is uninfected; and
- (f) identifying a trait present in said infected or uninfected host plant.

**REMARKS**

**The Amendments**

Claim 45 is amended to recite a method of determining the presence of a trait in a plant. Claim 45 is also amended to change the steps (e) and (f). Support for the amendments can be found in original Claims 4 and 6, which were canceled in response to a restriction requirement.

No new matter is added in any of the above amendments. The Examiner is requested to enter the amendments and reconsider the application.

**Remarks**

**1. 35 U.S.C. § 112, second paragraph rejection.**

Claims 45 and 60-70 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention. The rejections are overcome in view of the amendments.

The Examiner states that Claim 45 is vague and indefinite in that the metes and bounds of the phrase "functional gene profile" are unclear. Applicants have amended the claims to recite a method of determining the presence of a trait in a plant.

In view of the above amendments, the rejections of Claim 45 and Claims 60-70 should be withdrawn.



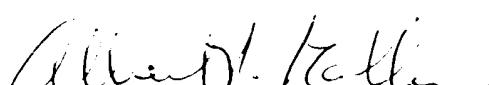
Application Serial No. 09/359,300  
Attorney's Docket No. 08010137US07

**CONCLUSION**

In view of the foregoing amendments and remarks, Applicants believe the application is in good and proper condition for allowance. If, in the opinion of the Examiner, a telephone conference would expedite the prosecution of the subject application, the Examiner is encouraged to call the undersigned at (650) 463-8109.

Respectfully submitted,

Date: June 21, 2002

  
Albert P. Halluin (Reg. No. 25,227)

Viola T. Kung (Reg. No. 41,131)

**HOWREY SIMON ARNOLD & WHITE, LLP.**  
301 Ravenswood Avenue  
Box No. 34  
Menlo Park, CA 94025-3435  
(650) 463-8109

RECEIVED

JUN 27 2002

TECH CENTER 1600/2900



Application No.: 09/359,300  
Attorney Docket No.: 00801.0137.US07

MARKED-UP VERSION TO SHOW CHANGES MADE IN THE CLAIMS

45. (Five Times Amended) A method of [compiling a positive sense functional gene profile of an organism] determining the presence of a trait in a plant, comprising:

- (a) preparing a library of DNA or RNA sequences from a non-plant donor organism, and constructing recombinant viral nucleic acids each comprising an unidentified nucleic acid insert obtained from said library in a positive sense orientation;
- (b) infecting plant hosts with said recombinant viral nucleic acids;
- (c) transiently expressing the unidentified nucleic acid inserts in said infected plant hosts;
- (d) determining one or more phenotypic or biochemical changes in said plant hosts;
- [(e) identifying said recombinant viral nucleic acids that result in said one or more phenotypic or biochemical changes in said plant host;
- (f) identifying donor genes or plant host genes associated with said one or more phenotypic or biochemical changes; whereby a positive sense functional gene profile of said plant host or said donor organism is compiled.]
- (e) correlating said one or more phenotypic or biochemical changes to a host plant that is uninfected; and
- (f) identifying a trait present in said infected or uninfected host plant.



Application No.: 09/359,300  
Attorney Docket No.: 00801.0137.US07

MARKED-UP VERSION TO SHOW CHANGES MADE IN THE TITLE

Page 1, lines 1-3:

METHOD OF [COMPILING A FUNCTIONAL GENE PROFILE] DETERMINING  
THE PRESENCE OF A TRAIT BY TRANSFECTING A NUCLEIC ACID SEQUENCE OF A  
NON-PLANT DONOR INTO A HOST PLANT IN A POSITIVE SENSE ORIENTATION.